

# FEE TRANSMITTAL for FY 2004

Effective 10/01/2003. Patent fees are subject to annual revision.

☒ Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT (\$) 385

## Complete if Known

Application Number \_\_\_\_\_  
 Filing Date March 11, 2004  
 First Named Inventor Gilbert, Michel  
 Examiner Name \_\_\_\_\_  
 Art Unit \_\_\_\_\_  
 Attorney Docket No. 019633-000912US

## METHOD OF PAYMENT (check all that apply)

☐ Check ☐ Credit Card ☐ Money Order ☐ Other ☐ None
☒ Deposit Account:Deposit  
Account  
Number

20-1430

Deposit  
Account  
Name

Townsend and Townsend and Crew LLP

The Director is authorized to: (check all that apply)

☒ Charge fee(s) indicated below ☒ Credit any overpayments☒ Charge any additional fee(s) or any underpayment of fee(s)☐ Charge fee(s) indicated below, except for the filing fee to the above-identified deposit account.

## FEE CALCULATION

## 1. BASIC FILING FEE

Large Entity	Small Entity	Fee Code	Fee (\$)	Fee Description	Fee Paid
		1001	770	2001 385 Utility filing fee	385
		1002	340	2002 170 Design filing fee	
		1003	530	2003 265 Plant filing fee	
		1004	770	2004 385 Reissue filing fee	
		1005	160	2005 80 Provisional filing fee	

SUBTOTAL (1)

(\$385)

## 2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE

Total Claims	Extra Claims	Fee from below	Fee Paid
16	-20** = 0	X\$9	\$0
Independent Claims	1	-3** = 0	X\$43
Multiple Dependent		X	

Large Entity	Small Entity	Fee Code	Fee (\$)	Fee Description
		1202	18	2202 9 Claims in excess of 20
		1201	86	2201 43 Independent claims in excess of 3
		1203	290	2203 145 Multiple dependent claim, if not paid
		1204	86	2204 43 ** Reissue independent claims over original patent
		1205	18	2205 9 ** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2)

(\$0)

\*\*or number previously paid, if greater; For Reissues, see above

## FEE CALCULATION (continued)

## 3. ADDITIONAL FEES

Large Entity	Small Entity	Fee Code	Fee (\$)	Fee Description	Fee Paid
		1051	130	2051 65 Surcharge - late filing fee or oath	
		1052	50	2052 25 Surcharge - late provisional filing fee or cover sheet.	
		1053	130	1053 130 Non-English specification	
		1812	2,520	1812 2,520 For filing a request for reexamination	
		1804	920*	1804 920* Requesting publication of SIR prior to Examiner action	
		1805	1,840*	1805 1,840* Requesting publication of SIR after Examiner action	
		1251	110	2251 55 Extension for reply within first month	
		1252	420	2252 210 Extension for reply within second month	
		1253	950	2253 475 Extension for reply within third month	
		1254	1,480	2254 740 Extension for reply within fourth month	
		1255	2,010	2255 1,005 Extension for reply within fifth month	
		1401	330	2401 165 Notice of Appeal	
		1402	330	2402 165 Filing a brief in support of an appeal	
		1403	290	2403 145 Request for oral hearing	
		1451	1,510	1451 1,510 Petition to institute a public use proceeding	
		1452	110	2452 55 Petition to revive - unavoidable	
		1453	1,330	2453 665 Petition to revive - unintentional	
		1501	1,330	2501 665 Utility issue fee (or reissue)	
		1502	480	2502 240 Design issue fee	
		1503	640	2503 320 Plant issue fee	
		1460	130	1460 130 Petitions to the Commissioner	
		1807	50	1807 50 Petitions related to provisional applications	
		1806	180	1806 180 Submission of Information Disclosure Stmt	
		8021	40	8021 40 Recording each patent assignment per property (times number of properties)	
		1809	770	2809 385 Filing a submission after final rejection (37 CFR § 1.129(a))	
		1810	770	2810 385 For each additional invention to be examined (37 CFR § 1.129(b))	
		1801	770	2801 385 Request for Continued Examination (RCE)	
		1802	900	1802 900 Request for expedited examination of a design application	

Other fee (specify) \_\_\_\_\_

\*Reduced by Basic Filing Fee Paid SUBTOTAL (3)

(\$)

## SUBMITTED BY

## Complete (if applicable)

Name (Print/Type) Beth L. Kelly Registration No. (Attorney/Agent) 51,868 Telephone 415-576-0200  
 Signature *Beth L. Kelly* Date March 11, 2004

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016/019

MAR 30 2007

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

GILBERT and WAKARCHUK

Application No.: 10/799,016

Filed: March 11, 2004

For: LIPOPOLYSACCHARIDE A-2,3  
SIALYLTRANSFERASE OF  
CAMPYLOBACTER JEJUNI AND ITS  
USES

Customer No.: 20350

Confirmation No. 7215

Examiner: Portner, Virginia Allen

Technology Center/Art Unit: 1645

TERMINAL DISCLAIMER

Mail Stop Amendment  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

Petitioner, National Research Council of Canada, Inc., is the owner of 100 percent interest in the instant application. Petitioner hereby disclaims, except as provided below, the terminal part of the statutory term of any patent granted on the instant application, which would extend beyond the expiration date of the full statutory term defined in 35 U.S.C. 154 to 156 and 173 as shortened by any terminal disclaimer filed prior to the grant of U.S. Patent No. 6,709,834 (filed January 29, 2002).

U.S. Patent No. 6,709,834 and the instant application were commonly owned at that time of invention of the subject matter claimed in U.S. Patent No. 6,709,834. Petitioner hereby agrees that any patent so granted on the instant application shall be enforceable only for and during such period that it and U.S. Patent No. 6,709,834 are commonly owned. This agreement runs with any patent granted on the instant application and is binding upon the grantee, its successors or assigns.

In making the above disclaimer, petitioner does not disclaim the terminal part of any patent granted on the instant application that would extend to the expiration date of the full

statutory term as deemed in 35 U.S.C. 154 to 156 and 173 of a patent granted from U.S. Patent No. 6,709,834, as shortened by any terminal disclaimer filed prior to the patent grant, in the event that any such patent: expires for failure to pay a maintenance fee, is held unenforceable, is found invalid by a court of competent jurisdiction, is statutorily disclaimed in whole or terminally disclaimed under 37 CFR 1.321, has all claims canceled by a reexamination certificate, is reissued, or is in any manner terminated prior to the expiration of its full statutory term as shortened by any terminal disclaimer filed prior to its grant.

For submissions on behalf of an organization (e.g., corporation, partnership, university, government agency, etc.), the undersigned (whose title is supplied below) is empowered to act on behalf of the organization.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Date: 26 March 2007

By: Marielle Piché  
Name: Marielle Piché

Title: Secretary General, EXECUTIVE OFFICES  
Secretary General, Executive Offices  
Secretariat

Executive Offices  
National Research Council of Canada  
1200 Montreal Road  
M-58 Room W-312  
Ottawa, ON K1A 0R6

BLK:blk  
61003220 v1

Appl. No. 10/799,016  
Amdt. dated March 29, 2007  
Amendment under 37 CFR 1.116 Expedited Procedure  
Examining Group 1645

**PATENT**

**Amendments to the Specification:**

Please replace paragraph beginning at page 9, line 18 with the following amended paragraph:

Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>) ([ncbi.nlm.nih.gov/](http://www.ncbi.nlm.nih.gov/)). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra.*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. For identifying whether a nucleic acid or polypeptide is within the scope of the invention, the default parameters of the BLAST programs are suitable. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).

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**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-34. (cancelled)

35. (Currently amended) An isolated  $\alpha$ -2,3-sialyltransferase polypeptide, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide catalyzes the transfer of a sialic acid from a donor substrate to an acceptor sugar, and wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises an the amino acid sequence with at least 90% identity to of residues 1-328 of SEQ ID NO:2, over the entire length of or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2.

36-37. (Cancelled)

38. (Currently amended) <sup>An isolated</sup> The  $\alpha$ -2,3-sialyltransferase polypeptide of claim 37, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises an the amino acid sequence with at least 95% identity to of residues 1-430 of SEQ ID NO:2, over the entire length of or an amino acid sequence that shares at least 95% identity with amino acid residues 1-430 of SEQ ID NO:2.

39. (Previously presented) The  $\alpha$ -2,3-sialyltransferase polypeptide of claim 35, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide further comprises an amino acid tag.

40. (Previously presented) The  $\alpha$ -2,3-sialyltransferase polypeptide of claim 39, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

41. (Previously presented) A method of adding a sialic acid residue to an acceptor molecule comprising a terminal galactose residue, the method comprising contacting

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**PATENT****Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-34. (cancelled)

<sup>1</sup> 35. (Currently amended) An isolated  $\alpha$ -2,3-sialyltransferase polypeptide, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide catalyzes the transfer of a sialic acid from a donor substrate to an acceptor sugar, and wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises an the amino acid sequence with at least 90% identity to of residues 1-328 of SEQ ID NO:2, over the entire length of or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2.

36-37. (Cancelled)

<sup>4</sup> 38. (Currently amended) <sup>An isolated</sup> ~~The~~  $\alpha$ -2,3-sialyltransferase polypeptide of claim 37, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises an the amino acid sequence with at least 95% identity to of residues 1-430 of SEQ ID NO:2, over the entire length of or an amino acid sequence that shares at least 95% identity with amino acid residues 1-430 of SEQ ID NO:2.

<sup>1</sup> 39. (Previously presented) The  $\alpha$ -2,3-sialyltransferase polypeptide of claim 35, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide further comprises an amino acid tag.

<sup>3</sup> 40. (Previously presented) The  $\alpha$ -2,3-sialyltransferase polypeptide of claim 39, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

<sup>5</sup> 41. (Previously presented) A method of adding a sialic acid residue to an acceptor molecule comprising a terminal galactose residue, the method comprising contacting

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the acceptor molecule with an activated sialic acid molecule and an  $\alpha$ -2,3-sialyltransferase polypeptide of claim 35 or claim ~~37~~ 38

42. (Previously presented) The method of claim 41, wherein the terminal galactose residue is linked through a linkage to a second residue in the acceptor molecule.

43. (Previously presented) The method of claim 42, wherein the linkage is a  $\beta$ 1,4 linkage.

44. (Previously presented) The method of claim 43, wherein the second residue is a Glc or a GlcNAc.

45. (Previously presented) The method of claim 42, wherein the linkage is a  $\beta$ 1,3 linkage.

46. (Previously presented) The method of claim 45, wherein the second residue is a GlcNAc or a GalNAc.

47. (Previously presented) The method of claim 41, wherein the activated sialic acid is CMP-Neu5Ac.

48. (Currently amended) The method of claim 41, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises ~~an the~~ amino acid sequence with at least 95% identity to ~~of residues 1-328 of SEQ ID NO:2, over the entire length of residues 1-328.~~

49. (Previously presented) The method of claim 41, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide further comprises an amino acid tag.

50. (Previously presented) The method of claim 49, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).

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the acceptor molecule with an activated sialic acid molecule and an  $\alpha$ -2,3-sialyltransferase polypeptide of claim ~~35~~ <sup>38</sup> or claim ~~36~~ <sup>4</sup>.

<sup>10</sup> ~~42~~ <sup>5</sup>. (Previously presented) The method of claim ~~41~~ <sup>5</sup>, wherein the terminal galactose residue is linked through a linkage to a second residue in the acceptor molecule.

<sup>11</sup> ~~43~~ <sup>10</sup>. (Previously presented) The method of claim ~~42~~ <sup>10</sup>, wherein the linkage is a  $\beta$ 1,4 linkage.

<sup>12</sup> ~~44~~ <sup>11</sup>. (Previously presented) The method of claim ~~43~~ <sup>11</sup>, wherein the second residue is a Glc or a GlcNAc.

<sup>13</sup> ~~45~~ <sup>10</sup>. (Previously presented) The method of claim ~~44~~ <sup>10</sup>, wherein the linkage is a  $\beta$ 1,3 linkage.

<sup>14</sup> ~~46~~ <sup>13</sup>. (Previously presented) The method of claim ~~45~~ <sup>13</sup>, wherein the second residue is a GlcNAc or a GalNAc.

<sup>6</sup> ~~47~~ <sup>5</sup>. (Previously presented) The method of claim ~~46~~ <sup>5</sup>, wherein the activated sialic acid is CMP-Neu5Ac.

<sup>7</sup> ~~48~~ <sup>5</sup>. (Currently amended) The method of claim ~~47~~ <sup>5</sup>, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises ~~an the amino acid sequence with at least 95% identity to of residues 1-328 of SEQ ID NO:2, over the entire length of residues 1-328.~~

<sup>8</sup> ~~49~~ <sup>5</sup>. (Previously presented) The method of claim ~~48~~ <sup>5</sup>, wherein the  $\alpha$ -2,3-sialyltransferase polypeptide further comprises an amino acid tag.

<sup>9</sup> ~~50~~ <sup>8</sup>. (Previously presented) The method of claim ~~49~~ <sup>8</sup>, wherein the amino acid tag is a member selected from the group consisting of polyhistidine, maltose binding protein, myc, V-5, and DYKDDDK (SEQ ID NO:8).



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**REMARKS/ARGUMENTS**

With this amendment, claims 35, and 38-50 are pending. Claims 1-34, 36, and 37 are cancelled. For convenience, the Examiner's rejections are addressed in the order presented in a November 8, 2006 Office Action.

**I. Status of the claims**

Claim 35 is amended to recite wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2. Claim 38 was similarly amended and recites amino acid residues 1-430. Support for these amendments is found throughout the specification, for example, at page 4, lines 17-20 and page 8, lines 26-30. These amendments add no new matter.

**II. Objections to the specification**

The Office Action objects to the presence of hyperlinks in the specification. In order to expedite prosecution, the specification is amended to remove hyperlinks. In view of the above amendments, withdrawal of the specification and drawing objections is respectfully requested.

**III. Rejections under 35 U.S.C. §112, first paragraph, written description**

Claims 35-50 are rejected under 35 U.S.C. §112, first paragraph for allegedly failing to comply with the written description requirement. According to the Office Action, the specification does not provide description of polypeptides with at least 90-95% identity to SEQ ID NO:2. The Office Action alleges that those of skill would not recognize that the inventors had possession of the claimed invention at the time of filing.

The Office Action indicates that the written description rejection can be obviated by amending the claims to recite "wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at

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least 95% identity with amino acid residues 1-328 of SEQ ID NO:2." See, i.e., Office Action at page 4. Applicants have amended claims 35 and 38 as suggested in the Office Action in order to expedite prosecution. It is Applicants' understanding that the amended claims overcome the rejections for alleged lack of written description. In view of these amendments and remarks, withdrawal of the rejection under 35 U.S.C. §112, first paragraph is respectfully requested.

**IV. Rejections under 35 U.S.C. §102(b) and §102(e)**

Claims 35-39 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by Gilbert *et al.* *J. Biol. Chem.* 271:28217-28276 (1996) and under 35 U.S.C. §102(b) by Paulson *et al.* (U.S. Patent No. 6,399,336).

To anticipate a claim, the reference must teach every element of the claim. "A claim is anticipated only if each and every element as set forth in the claim is found...in a single prior art reference." *Verdegaal Bros. v. Union Oil of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987). Thus, in order to anticipate, the cited reference must contain every element of the claims at issue.

Applicants respectfully traverse the rejection and submit that, as amended, the claims are not anticipated by the cited references. Moreover, the Office Action indicates that the anticipation rejections can be obviated by amending the claims to recite "wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2." See, i.e., Office Action at page 5. In view of these amendments and remarks, withdrawal of the rejection under 35 U.S.C. §102 is respectfully requested.

**V. Rejections for alleged obviousness-type double patenting**

Claim 35-47 and 49-50 are rejected as allegedly unpatentable under the judicial doctrine of obviousness type double patenting over claims 1-15 of U.S. Patent No. 6,709,834. In order to expedite prosecution of this application, Applicants submit a terminal disclaimer of the term of a patent granted on the instant application over U.S. Patent No. 6,709,834. Applicants

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note that the filing of a terminal disclaimer to obviate a rejection based on non-statutory double patenting is not an admission of the propriety of the rejection. See, MPEP §804.02.

Accordingly, Applicants respectfully request withdrawal of this rejection.

Claims 35-40 are rejected for alleged obviousness-type double patenting over claims 43-46 of USSN 10/821,573, now US Patent No. 7,192,756 (the '756 patent), to be issued March 2007. Applicants respectfully traverse the rejection. The '756 patent claims CstII proteins that are encoded by a nucleic acid that is amplified from a *Campylobacter* genome using SEQ ID NOs:46 and 47 as the amplification primers. The present claims are directed to CstI proteins from *Campylobacter* bacteria. Applicants provide data that SEQ ID NOs:46 and 47 of the '756 patent will not amplify a nucleic acid from a *Campylobacter* genome that encodes the claimed proteins. Exhibit A provides alignments of the nucleic acid sequence of SEQ ID NO:1 from the present application with the nucleic acid sequence of SEQ ID NO:46 and the reverse complement of SEQ ID NO:47 from the '756 patent. SEQ ID NO:46 aligns poorly near the 5' end of SEQ ID NO:1 and substantial gaps are required for the alignment. Moreover, any amplified product would not include the initiating ATG codon. The reverse complement of SEQ ID NO:47 aligns poorly to SEQ ID NO:1, beginning at about nucleotide 742, and also requires substantial gaps to produce an alignment. Even if the sequence alignment and complementation was sufficient to allow hybridization and amplification of a nucleic acid product, that product would end at about nucleotide 797, or about encoded amino acid 265 of the claimed CstI polypeptides. The amended claims are directed to CstI polypeptides comprising 1-328 or 1-430 amino acids of SEQ ID NO:2 and proteins with 95% identity to those sequences. Thus, the '756 patent primers (SEQ ID NO:46 and 47) cannot be used to produce a nucleic acid that would encode the claimed functional CstI polypeptides. The polypeptides claimed by the present application and the '756 patent are, therefore, patentably distinct and this rejection for alleged obviousness-type double patenting should be withdrawn.

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Intc  
4/11/07  
REF 1497  
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**VI. Rejections under 35 U.S.C. §112, second paragraph**

Claims 35-50 are rejected because the phrase "over the entire length" is allegedly indefinite. Applicants respectfully traverse the rejection and submit that, as amended, the claims are not indefinite. Moreover, the Office Action indicates that the rejections for alleged indefiniteness can be obviated by amending the claims to recite "wherein the  $\alpha$ -2,3-sialyltransferase polypeptide comprises the amino acid sequence of residues 1-328 of SEQ ID NO:2 or an amino acid sequence that shares at least 95% identity with amino acid residues 1-328 of SEQ ID NO:2." See, i.e., Office Action at page 7. In view of these amendments and remarks, withdrawal of the rejection for alleged indefiniteness is respectfully requested.

**CONCLUSION**

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

  
Beth L. Kelly  
Reg. No. 51,868

TOWNSEND and TOWNSEND and CREW LLP  
Two Embarcadero Center, Eighth Floor  
San Francisco, California 94111-3834  
Tel: 415-576-0200  
Fax: 415-576-0300  
Attachments  
BLK:blk  
60981816 v1

Needle

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## EMBOSS Align Results

Needle Results	
Matrix	Blosum82
Open gap penalty	10.0
Gap extension penalty	0.5
Needle output	needle-20070308-23144402448256.output
SUBMIT ANOTHER JOB	

```
#####
# Program: needle
# Rndate: Thu Mar 08 23:14:44 2007
# Align_format: srspair
# Report_file: /ebi/extern/old-work/needle-20070308-23144402448256.output
#####
```

```
#=====
#
# Aligned sequences: 2
# 1: seq 1 from present app
# 2: rev 47 from '756 patent
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1293
# Identity: 28/1293 ( 2.2%)
# Similarity: 28/1293 ( 2.2%)
# Gaps: 1252/1293 (96.8%)
# Score: 110.0
#
#=====
```

seq	1	atgacaaggactagatggaaaatgaactcattgtagtaaaaatatgca	50
rev	1		0
seq	51	aaatataatcatagcaggaatggacctagcctaaaaaatattaattata	100
rev	1		0
seq	101	aaagactgcctagagaatatgatgttttaggtgtaaccagttttatctt	150
rev	1		0
seq	151	gaagataagcattatttaggaaaaagattaaagcagtattttttaatcc	200
rev	1		0
seq	201	tgggtgtctttttacacagtatcacactgcaaaacaacttatactaaaaa	250
rev	1		0
seq	251	atgagtatgaaataaaaaatattttttgcctctacatttaattacctttt	300
rev	1		0

EXHIBIT

A

Needle

Page 2 of 3

seq	301	attgaaagcaatgattttttacatcaattttataattttttcccgatgc	350
rev	1		0
seq	351	aaaacttggctatgaagttattgaaaacccaaagaattttatgcttata	400
rev	1		0
seq	401	taaaatacaatgaaatttcatttcaataaaagaattacttcgggcgtctat	450
rev	1		0
seq	451	atgtgtgcaattgctattgcattaggatataaaaccatctatttatgtgg	500
rev	1		0
seq	501	cattgatttttatgaaggagatggtattttatccctttgaagctatgagca	550
rev	1		0
seq	551	caaataataaaaacaatctttcctggaaataaaagatttcaaacccttcaaat	600
rev	1		0
seq	601	tgtcatttctaaggaatacgaatagagaagcattaaaattgttaaatcaat	650
rev	1		0
seq	651	atacaaagttaatatctacgcattgtgtgatgattctatttcggcaaatc	700
rev	1		0
seq	701	attttcctttatcaattaatattaataacaattttcaotttagaaaaataag	750
rev	1		9
seq	751	cataataattctataaatgatattttattgactgataataactcctggcgt	800
rev	10	<div style="display: flex; justify-content: space-between;"> <div> <div style="text-align: center;">   </div> <div style="text-align: center;">   .   </div> <div style="text-align: center;">   .   .   .   .   </div> <div style="text-align: center;">   .   </div> </div> <div> <div style="text-align: center;">GATATAAAG</div> </div> </div>	41
seq	801	aagtttttataaaaatcaacttaagctgataataaaattatgcttaatt	850
rev	42		41
seq	851	tttataatattcttcattctaagataatttaattcaaatctttaaacaaa	900
rev	42		41
seq	901	gaaattgcggtatttaaaaaaacaaccactcaacgagctaaagcaagaat	950
rev	42		41
seq	951	ccaaaaccatctatcctataaaactaggacaagctttgattataaattcta	1000
rev	42		41
seq	1001	aaagtgtattagggtttttatctttacctcttataatattaagtatcggt	1050
rev	42		41
seq	1051	atttcacataaacaagaacaaaaggcttataaaatttaagtaaaagaaaa	1100
rev	42		41
seq	1101	tccaaatttagctttacctcctttagaacttatcctgattataatgaag	1150

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rev	42		41
seq	1151	cttctaaaagaaaaagaatgttttactttatanaattaggagaagaatttata	1200
rev	42		41
seq	1201	aaagctggtaagaattgggtatggggaggggtatatcaaatcttatccaa	1250
rev	42		41
seq	1251	agatgttccttaggttgaagagagagtttgagaaaggggaataa	1293
rev	42		41

#-----  
#-----

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## Needle Results

**SUBMIT ANOTHER JOB**

```

#####
#
# Aligned sequences: 2
# 1: seq 7 from present application
# 2: seq 46 from '756 patent
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1293
# Identity:      28/1293 ( 2.2%)
# Similarity:    28/1293 ( 2.2%)
# Gaps:          1252/1293 (96.8%)
# Score: 130.0
#
#
#####

```

PAGE 13/19 \* RCVD AT 3/30/2007 12:35:44 PM [Eastern Daylight Time] \* SVR:USPTO-EFXRF-1/3 \* DNIS:2738300 \* CSID:415 576 0300 \* DURATION (mm:ss):05:262007



## Needle

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seq	301	attgaaagcaatgattttttacatcaattttataatctttcccgatgc	350
seq	42		41
seq	351	aaaacttggtatgaagctattgaaaaccttaagaattttatgcttata	400
seq	42		41
seq	401	taaaatacaatgaattttatttcaataaaagaattacttcgggcgtctat	450
seq	42		41
seq	451	atgtgtgcaattgctattgcattaggatataaaacctctattttatgtgg	500
seq	42		41
seq	501	cattgatttttatgaaggagatgttatttatccttttgaagctatgagta	550
seq	42		41
seq	551	caaatataaaaacaatctttcctggaataaaagatttcaaaccttcaaat	600
seq	42		41
seq	601	tgtcattctaagggaatacgcataagaagcattaaaattgttaaaatcaat	650
seq	42		41
seq	651	atacaaagttaatatctacgcattgtgtgatgattctattttggcaaarc	700
seq	42		41
seq	701	attttcctttatcaattaatattaataacaatttcacttttagaaaaaag	750
seq	42		41
seq	751	cataataattctataaatgatattttattgactgataatactcctggcgt	800
seq	42		41
seq	801	aagttttataaaaatcaacttaagctgataataaaattatgcttaatt	850
seq	42		41
seq	851	tttataatattcttcattctaaagataatttaattaaatttttaaacaaa	900
seq	42		41
seq	901	gaaattgcggtatttaaaaaacaaaccactcaacgagctaaagcaagaat	950
seq	42		41
seq	951	ccaaaaccatctatcctataaaactaggacaagctttgattataaattcta	1000
seq	42		41
seq	1001	aaagtgtattaggttttttatctttaccttttataataatcaagtatcgtt	1050
seq	42		41
seq	1051	atttoacataaacaagaacaaaaggcttataaatttaagtaaaagaaaaa	1100
seq	42		41
seq	1101	tccaaatctagctttacctccttttagaaacttatcctgattataatgaag	1150

Needle

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seq	42		41
seq	1151	ctttaaaagaaaaagaatgttttactttataaattaggagaagaattttata	1200
seq	42		41
seq	1201	aaagctggtaagaattggatggggaggggcataacaaatttatattcaa	1250
seq	42		41
seq	1251	agatgttcctaggttgaagagagagcttgagaaaggggaataa	1293
seq	42		41

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